

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of claims:

Claims 1-45 (cancelled).

Claim 46 (currently amended): A method of making a nucleic acid ~~having a modified for~~
~~modifying a base sequence of a gene for transforming a plant, comprising modifying a gene of~~
~~another species by the sequence of the gene in accordance with~~ features (A) and (B) without
altering the amino acid sequence thereof, ~~in order to avoid for eliminating sequences relating to~~
poly(A) addition,

wherein features (A) and (B) are defined as follows:

(A) ~~eliminating~~ GT rich regions comprising 8 or more consecutive bases of G or T within the
coding region of the gene ~~are eliminated~~,

and

(B) ~~eliminating~~ sequences encoded by AATAAA, NATAAA, ANTAAA, AANAAA,
AATNAA, AATANA, or AATAAN within the coding region of the gene ~~are eliminated~~.

Claim 47 (previously presented): The method of making the nucleic acid according to claim 46,
wherein the gene is derived from yeast.

Claim 48 (previously presented): The method of making the nucleic acid according to claim 46,
wherein the gene derived from yeast is a ferric-chelate reductase gene.

Claim 49 (previously presented): The method of making the nucleic acid according to claim 46,
wherein codon usage of the base sequence is modified to increase a preferred codon of the plant.

Claim 50 (previously presented): The method of making the nucleic acid according to claim 46,
wherein there is no observable difference in content between base G and base C throughout the

gene to be introduced.

Claim 51 (previously presented): The method of making the nucleic acid according to claim 46, wherein the base sequence is optimized such that ATTTA sequences are eliminated, without altering the amino acid sequence.

Claim 52 (previously presented): The method of making the nucleic acid according to claim 46, wherein the base sequence located upstream of the gene's initiation codon is altered to a sequence for effective translation of mRNA known as Kozak sequence.

Claim 53 (previously presented): The method of making the nucleic acid according to claim 46, wherein the nucleic acid is DNA.

Claim 54 (previously presented): The method of making the nucleic acid according to claim 53, wherein the DNA has a base sequence as set forth in SEQ ID NO: 1.

Claim 55 (previously presented): A nucleic acid having a modified base sequence of a ferric-chelate reductase gene derived from *Saccharomyces cerevisiae* FRE1, wherein the sequence is modified by features (A) and (B) without altering the amino acid sequence thereof, for eliminating the sequences relating to poly(A) addition, and for introducing said gene into a plant, wherein features (A) and (B) are defined as follows:

- (A) GT rich regions comprising 8 or more consecutive bases of G or T are eliminated, and
- (B) sequences encoded by AATAAA, NATAAA, ANTAAA, AANAAA, AATNAA, AATANA, or AATAAN are eliminated.

Claim 56 (previously presented): The DNA according to claim 55, wherein the DNA has a base sequence as set forth in SEQ ID NO: 1.